

Nucleotide Sequence of Human ABCG4 Transporter Gene

GCCACCATGG	CGGAGAAGGC	GCTGGAGGCC	GTGGGCTGTG	GACTAGGGCC	GGGGGCTGTG	60
GCCATGGCCG	TGACGCTGGA	GGACGGGGCG	GAACCCCTG	TGCTGACCAC	GCACCTGAAG	120
AAGGTGGAGA	ACCACATCAC	TGAAGCCCAG	CGTTTCTCCC	ACCTGCCCAA	GCGCTCAGCC	180
GTGGACATCG	AGTTCGTGGA	GCTGTCTTAT	TCCGTGCGGG	AGGGGCCCTG	CTGGCGCAAA	240
AGGGGTTATA	AGACCCTTCT	CAAGTGCCTC	TCAGGTAAT	TCTGCCGCCG	GGAGCTGATT	300
GGCATCATGG	GCCCCTCAGG	GGCTGGCAAG	TCTACATTCA	TGAACATCTT	GCGAGGATAC	360
AGGAGTCTG	GAATGAAGGG	GCAGATCTCT	GTTAATGGAA	GGACATCGGA	GCTGAGGACC	420
TTCCGCAAGA	TGTTCTGTCT	CATCATGCAA	GATGACATGC	TGCTGCCGCA	CCTCACGGTG	480
TTGGAAGCCA	TGATGGTCTC	TGCTAACCTG	AATCTTACTG	AGAATCCCGA	TGTGAAAAAC	540
GATCTCGTGA	CAGAGATCCT	GACGGCACTG	GGCCTGATGT	CGTGCTCCCA	CACGAGGACA	600
GCCCTGCTCT	CTGGCGGGCA	GAGGAAGCGT	CTGGCCATCG	CCCTGGAGCT	GGTCAACAAAC	660
CCGCCTGTCA	TGTTCTTTGA	TGAGCCCACC	AGTGGTCTGG	ATAGCGCCTC	TTGTTTCCAA	720
GTGGTGTCCC	TCATGAAGTC	CCTGGCACAC	GGGGGCCGTA	CCATCATCTG	CACCATCCAC	780
CAGCCCAGTC	CCAAGCTCTT	TGAGATGTTT	GACAAGCTCT	ACATCTTGAG	CAGGGTCTAG	840
TGCACTTTCA	AAGGAGTGGT	CACCAACCTG	ATCCCCTATC	TAAAGGGACT	CGGCTTGCAT	900
TGCCCCACCT	ACCACAACCC	GGCTGACTTC	ATCATCGAGG	TGGCCTCTGG	CGAGTATGGA	960
GACCTGAACC	CCATGTTGTT	CAGGGCTGTG	CAGAATGGGC	TGTGCGCTAT	GGCTGAGAAG	1020
AAGAGCAGCC	CTGAGAAGAA	CGAGGTCCCT	GCCCCATGCC	CTCCTTGTC	TCCGGAAGTG	1080
GATCCCATTG	AAAGCCACAC	CTTTGCCACC	AGCACCCCTCA	CACAGTTCTG	CATCCTCTTC	1140
AAGAGGACCT	TCCTGTCCAT	CCTCAGGGAC	ACGGTCCCTGA	CCCACCTACG	TTTCATGTCC	1200
CACGTGGTTA	TTGGCGTGCT	CATCGGCCCT	CTCTACCTGC	ATATTGGCGA	CGATGCCAGC	1260
AAGGTCTTCA	ACAACACCGG	CTGCCTCTTC	TTCTCCATGC	TGTTCTTCAT	GTTTCGCCGC	1320
CTCATGCCAA	CTGTGCTCAC	CTTCCCCTTA	GAGATGGCGG	TCTTCATGAG	GGAGCACCTC	1380
AACTACTGGT	ACAGCCTCAA	AGCGTATTAC	CTGGCCAAGA	CCATGGCTGA	CGTGCCCTTT	1440
CAGTGGGTGT	GTCCGGTGGT	CTACTGCAGC	ATTGTGTACT	GGATGACGGG	CCAGCCCCGT	1500
GAGACCAGCC	GCTTCCTGCT	CTTCTCAGCC	CTGGCCACCG	CCACCGCCCT	GGTGGCCCCA	1560
TCCTTTGGGG	TGCTATCGG	AGCTGCTTCC	AACTCCCTAC	AGGTGGCCCT	TTTTGTGGGC	1620
CCAGTTACCG	CATCCCTGT	CTCTTGTTTC	TCCGGCTTCT	TTGTGAGCTT	CAAGACCATC	1680
CCCACTTACC	TGCAATGGAG	CTCCTATCTC	TCCTATGTCA	GGTATGGCTT	TGAGGGTGTG	1740
ATCCTGACGA	TCTATGGCAT	GGAGCGAGGA	GACCTGACAT	GTTTAGAGGA	ACGCTGCCCG	1800
TTCCGGGAGC	CACAGAGCAT	CCTCCGAGCG	CTGGATGTGG	AGGATGCCAA	GCTCTACATG	1860
GACTTCCTGG	TCTTGGGCAT	CTTCTTCTTA	GCCCTGCGGC	TGCTGGCCTA	CCTTGTGCTG	1920
CGTTACCGGG	TCAAGTCAGA	GAGATAGAGG	CTTGCCCAAG	CCTGTACCCC	AGCCCCGCA	1980
CGAGGAAGCC	CCGAGTCCCA	GCCCTTTGGG	ACTGTTTTAA	CCTTATAGAC	TTGGGCACTG	2040
GTTCTGTGGC	GGGCTATCCT	CTCTCCCTT	GGCTCCTCCA	CAGGCTGGCT	CTCGGACTGC	2100
GCTCCAGGCC	TGGGCTCTGG	GAGTGGGGGC	TCCAGCCCTC	CCCACTATGC	CCAGGAGTCT	2160
TCCCAAGTTG	ATGCGGTTTG	TAGCTTCTCT	CCTACTCTCT	CCAACACCTG	CATGCAAAGA	2220
CTACTGGGAG	GCTGCTGCCT	CCTTCTGCCC	CATGGCACCC	TCCTCTGCTG	TCTGCCTGGG	2280
AGCCCTAGGC	TCTCTAGGGC	CCCACTTACA	ACTGACCAAA	GTGGCCCCCT	CTGGGGGTCC	2340
CCACCAACA	AGTGTTTGTA	AACTGGGCTG	CTATAAGGTT	GGAGTTCACG	GGCTGGGCC	2400
TGGTGGAGTC	CCTGGAAGT	CCCATATAGG	ATGTTGAAT	TGGACGGGAA	GGACTCTGGA	2460
AGTCTCTTCC	TCTTCTCTCT	CTTCTCTCCA	CTGTTAGACC	CTGGCTGACT	TGGACAATCT	2520
GCCAGGACAG	AAGCTGGGTT	TTCTGTCTAG	GTCACCACTC	CCAATCCTGG	GGATTGGAGA	2580
GGCCTGGGGC	TGTGGGATGC	CCCATCCCCC	TCCCCATCAC	CTTTGGTGGG	GGCAGGGCCT	2640
GGTGGCACCT	GTGCAATAAT	GTCGTGTGTT	CTCTCCCACC	TGCCACTGGA	ACTGGAGAAT	2700
GCACTTTATT	CTGGGCGGGG	GGTGAGTGGG	GGAAGACCCA	ACCCTCCTTT	CTCGCTGCC	2760
CTAACGCATG	CACGGTCTCG	TGATGCTCTC	TCCCTCTCCG	GAGTGACAGG	CACATACATG	2820
AGAAACAGCC	ATCTGACCCC	TACACACTTG	CCATCCCCTA	CAGCAGACAG	GAAAGATGAT	2880
GGTGGCATGC	TGTTGGTGGC	GGGTGCTGGT	GGGAGGACAG	TGCCAACCTC	CTCCTGGGGA	2940

FIGURE 1B

TCCCATGTTG GAGACTCTAA GGATAAGGCT GGTGCTGCCC AGGGTGTCTA CAGGAACTGC 3000
AGGTGTCTAC CCCCAAGTCT TCCCTCCTCC CAAGCCAGGG GTGGCACAGG GCACTAGATC 3060
CCTGGAGTTC AGGAACCAAC ACAAGCACAA CCACGGGCAT AAGTTGGCCT TGGCCACTGC 3120
CACCCACGGC CCTCCTTTTG TGCTCCATGC TGGCATCTTC ACTCCCCTAC CCCTTCCCCA 3180
GCCACTGCTG CTCATTCAAA CTTCTGTCCA TGTCCCTCCA CTGTTCTTAT CAGCAGGTGG 3240
CCCCTGGGCA TCAGAACAGC CTGCCCTGGG CACCAGGTGG CAGACACACT CAGAGCATGT 3300
CTGGCTTTCC TGGTGGGTCC AGGCTCATTG TGCTTCTGAT TTCCCCTCCC CCAGGGCTCA 3360
TTTTCCCCCT TTTTCCTGTA CACATCCCTG TCTACCTCCT CTCACCCTGC CACAGATTCT 3420
TCCTATCACA CAGGGATGCC AGTTGTATTT GTGGG 3455

201003-03014

FIGURE 2A

Coding Sequence of Human ABCG4 Transporter Gene

Sequence Range: 1 to 3455

gcc acc atg gcg gag aag gcg ctg gag gcc gtg ggc tgt gga cta ggg ccg ggg gct gtg 60
Met Ala Glu Lys Ala Leu Glu Ala Val Gly Cys Gly Leu Gly Pro Gly Ala Val

gcc atg gcc gtg acg ctg gag gac ggg gcg gaa ccc cct gtg ctg acc acg cac ctg aag
120

Ala Met Ala Val Thr Leu Glu Asp Gly Ala Glu Pro Pro Val Leu Thr Thr His Leu Lys

aag gtg gag aac cac atc act gaa gcc cag cgc ttc tcc cac ctg ccc aag cgc tca gcc
180

Lys Val Glu Asn His Ile Thr Glu Ala Gln Arg Phe Ser His Leu Pro Lys Arg Ser Ala

gtg gac atc gag ttc gtg gag ctg tcc tat tcc gtg cgg gag ggg ccc tgc tgg cgc aaa
240

Val Asp Ile Glu Phe Val Glu Leu Ser Tyr Ser Val Arg Glu Gly Pro Cys Trp Arg Lys

agg ggt tat aag acc ctt ctc aag tgc ctc tca ggt aaa ttc tgc cgc cgg gag ctg att
300

Arg Gly Tyr Lys Thr Leu Leu Lys Cys Leu Ser Gly Lys Phe Cys Arg Arg Glu Leu Ile

ggc atc atg ggc ccc tca ggg gct ggc aag tct aca ttc atg aac atc ttg gca gga tac
360

Gly Ile Met Gly Pro Ser Gly Ala Gly Lys Ser Thr Phe Met Asn Ile Leu Ala Gly Tyr

agg gag tct gga atg aag ggg cag atc ctg gtt aat gga agg cca cgg gag ctg agg acc
420

Arg Glu Ser Gly Met Lys Gly Gln Ile Leu Val Asn Gly Arg Pro Arg Glu Leu Arg Thr

ttc cgc aag atg tcc tgc tac atc atg caa gat gac atg ctg ctg ccg cac ctc acg gtg
480

Phe Arg Lys Met Ser Cys Tyr Ile Met Gln Asp Asp Met Leu Leu Pro His Leu Thr Val

ttg gaa gcc atg atg gtc tct gct aac ctg aat ctt act gag aat ccc gat gtg aaa aac
540
Leu Glu Ala Met Met Val Ser Ala Asn Leu Asn Leu Thr Glu Asn Pro Asp Val Lys Asn
gat ctc gtg aca gag atc ctg acg gca ctg ggc ctg atg tgc tgc tcc cac acg agg aca
600
Asp Leu Val Thr Glu Ile Leu Thr Ala Leu Gly Leu Met Ser Cys Ser His Thr Arg Thr
gcc ctg ctc tct ggc ggg cag agg aag cgt ctg gcc atc gcc ctg gag ctg gtc aac aac
660
Ala Leu Leu Ser Gly Gly Gln Arg Lys Arg Leu Ala Ile Ala Leu Glu Leu Val Asn Asn
ccg cct gtc atg ttc ttt gat gag ccc acc agt ggt ctg gat agc gcc tct tgt ttc caa
720
Pro Pro Val Met Phe Phe Asp Glu Pro Thr Ser Gly Leu Asp Ser Ala Ser Cys Phe Gln
gtg gtg tcc ctc atg aag tcc ctg gca cag ggg ggc cgt acc atc atc tgc acc atc cac
780
Val Val Ser Leu Met Lys Ser Leu Ala Gln Gly Gly Arg Thr Ile Ile Cys Thr Ile His
cag ccc agt gcc aag ctc ttt gag atg ttt gac aag ctc tac atc ctg agc cag ggt cag
840
Gln Pro Ser Ala Lys Leu Phe Glu Met Phe Asp Lys Leu Tyr Ile Leu Ser Gln Gly Gln
tgc atc ttc aaa gga gtg gtc acc aac ctg atc ccc tat cta aag gga ctc ggc ttg cat
900
Cys Ile Phe Lys Gly Val Val Thr Asn Leu Ile Pro Tyr Leu Lys Gly Leu Gly Leu His
tgc ccc acc tac cac aac ccg gct gac ttc atc atc gag gtg gcc tct ggc gag tat gga
960
Cys Pro Thr Tyr His Asn Pro Ala Asp Phe Ile Ile Glu Val Ala Ser Gly Glu Tyr Gly
gac ctg aac ccc atg ttg ttc agg gct gtg cag aat ggg ctg tgc gct atg gct gag aag
1020
Asp Leu Asn Pro Met Leu Phe Arg Ala Val Gln Asn Gly Leu Cys Ala Met Ala Glu Lys
aag agc agc cct gag aag aac gag gtc cct gcc cca tgc cct cct tgt cct ccg gaa gtg
1080
Lys Ser Ser Pro Glu Lys Asn Glu Val Pro Ala Pro Cys Pro Pro Cys Pro Pro Glu Val

FIGURE 2C

gat ccc att gaa agc cac acc ttt gcc acc agc acc ctc aca cag ttc tgc atc ctc ttc
1140
Asp Pro Ile Glu Ser His Thr Phe Ala Thr Ser Thr Leu Thr Gln Phe Cys Ile Leu Phe

aag agg acc ttc ctg tcc atc ctc agg gac acg gtc ctg acc cac cta cgg ttc atg tcc
1200
Lys Arg Thr Phe Leu Ser Ile Leu Arg Asp Thr Val Leu Thr His Leu Arg Phe Met Ser

cac gtg gtt att ggc gtg ctc atc ggc ctc ctc tac ctg cat att ggc gac gat gcc agc
1260
His Val Val Ile Gly Val Leu Ile Gly Leu Leu Tyr Leu His Ile Gly Asp Asp Ala Ser

aag gtc ttc aac aac acc ggc tgc ctc ttc ttc tcc atg ctg ttc ctc atg ttc gcc gcc
1320
Lys Val Phe Asn Asn Thr Gly Cys Leu Phe Phe Ser Met Leu Phe Leu Met Phe Ala Ala

ctc atg cca act gtg ctc acc ttc ccc tta gag atg gcg gtc ttc atg agg gag cac ctc
1380
Leu Met Pro Thr Val Leu Thr Phe Pro Leu Glu Met Ala Val Phe Met Arg Glu His Leu

aac tac tgg tac agc ctc aaa gcg tat tac ctg gcc aag acc atg gct gac gtg ccc ttt
1440
Asn Tyr Trp Tyr Ser Leu Lys Ala Tyr Tyr Leu Ala Lys Thr Met Ala Asp Val Pro Phe

cag gtg gtg tgt ccg gtg gtc tac tgc agc att gtg tac tgg atg acg ggc cag ccc gct
1500
Gln Val Val Cys Pro Val Val Tyr Cys Ser Ile Val Tyr Trp Met Thr Gly Gln Pro Ala

gag acc agc cgc ttc ctg ctc ttc tca gcc ctg gcc acc gcc acc gcc ttg gtg gcc caa
1560
Glu Thr Ser Arg Phe Leu Leu Phe Ser Ala Leu Ala Thr Ala Thr Ala Leu Val Ala Gln

tct ttg ggg ctg ctg atc gga gct gct tcc aac tcc cta cag gtg gcc act ttt gtg ggc
1620
Ser Leu Gly Leu Leu Ile Gly Ala Ala Ser Asn Ser Leu Gln Val Ala Thr Phe Val Gly

cca gtt acc gcc atc cct gtc ctc ttg ttc tcc ggc ttc ttt gtc agc ttc aag acc atc
1680

Pro Val Thr Ala Ile Pro Val Leu Leu Phe Ser Gly Phe Phe Val Ser Phe Lys Thr Ile
ccc act tac ctg caa tgg agc tcc tat ctc tcc tat gtc agg tat ggc ttt gag ggt gtg
1740
Pro Thr Tyr Leu Gln Trp Ser Ser Tyr Leu Ser Tyr Val Arg Tyr Gly Phe Glu Gly Val
atc ctg acg atc tat ggc atg gag cga gga gac ctg aca tgt tta gag gaa cgc tgc ccg
1800
Ile Leu Thr Ile Tyr Gly Met Glu Arg Gly Asp Leu Thr Cys Leu Glu Glu Arg Cys Pro
ttc cgg gag cca cag agc atc ctc cga gcg ctg gat gtg gag gat gcc aag ctc tac atg
1860
Phe Arg Glu Pro Gln Ser Ile Leu Arg Ala Leu Asp Val Glu Asp Ala Lys Leu Tyr Met
gac ttc ctg gtc ttg ggc atc ttc ttc cta gcc ctg cgg ctg ctg gcc tac ctt gtg ctg
1920
Asp Phe Leu Val Leu Gly Ile Phe Phe Leu Ala Leu Arg Leu Leu Ala Tyr Leu Val Leu
cgt tac cgg gtc aag tca gag aga tag agg ctt gcc cca gcc tgt acc cca gcc cct gca
1980
Arg Tyr Arg Val Lys Ser Glu Arg ***
gca gga agc ccc cag tcc cag ccc ttt ggg act gtt tta acc tta tag act tgg gca ctg
2040
gtt cct ggc ggg gct atc ctc tcc tcc ctt ggc tcc tcc aca ggc tgg ctg tcg gac tgc
2100
gct ccc agc ctg ggc tct ggg agt ggg ggc tcc agc cct ccc cac tat gcc cag gag tct
2160
tcc caa gtt gat gcg gtt tgt agc ttc ctc cct act ctc tcc aac acc tgc atg caa aga
2220
cta ctg gga ggc tgc tgc ctc ctt cct gcc cat ggc acc ctc ctc tgc tgt ctg cct ggg
2280
agc cct agg ctc tct agg gcc cca ctt aca act gac caa agt ggc ccc ctc tgg ggg tcc
2340
cca cca cac aag tgt ttg taa act ggg ctg cta taa ggt tgg agt tcc agg gct ggg ccc
2400

FIGURE 2E

tgg tgg agt cca ctg gaa gtc cca tta tgg atg ttg aaa tgg aca ggg aag gac tct gga
2460
agt ctc ttc ctc ctc ctc ttc tct cca ccc cta gac cct ggc tga ctt gga caa tct
2520
gcc agg aca gaa gct ggg ttt tct gtc tag gtc acc act ccc aat cct ggg gat tgg aga
2580
ggc ctg ggg ctg tgg gat gcc cca tcc ccc tcc cca tca cct ttg gtg ggg gca ggg cct
2640
ggt ggc acc tgt gca ata atg tct gtg ttt ctc tcc cac ctg cca ctg gaa ctg gag aat
2700
gca ctt tat tct ggg cgg ggg gtg agt ggg gga aga ccc aac cct cct ttc tcg ctg ccc
2760
cta acg cat gca cgg tct cgt gat gct ccc tcc ctc tcc gga gtg aca ggc aca tac atg
2820
aga aca ggc cat ctc agc cct aca cac ttg cca tcc cct aca gca cag agg aag agt gat
2880
ggt ggc atg ctg gtg gtg gcg ggt gct ggt ggg agg aca gtg cca acc tcc tcc tgg gga
2940
tcc cat gtt gga gac tct aag gat aag gct ggt gct gcc cag ggt gtc tac agg aac tgc
3000
agg tgt cta ccc cca agt ctt ccc tcc tcc caa gcc agg ggt ggc aca ggg cac tag atc
3060
cct gga gtt cag gaa cca aca caa gca caa cca cgg gca taa gtt ggc ctt ggc cac tgc
3120
cac cca cgg ccc tcc ttt tgt gct cca tgc tgg cat ctt cac tcc cct acc cct tcc cca
3180
gcc act gct gct cat tca aac ttc tgt cca tgt ccc tcc act gtt cct atc agc agg tgg
3240
ccc ctg ggc atc aga aca gcc tgc cct ggg cac cag gtg gca gac aca ctc aga gca tgt
3300
ctg gct ttc ctg gtg ggt cca ggc tca ttc tgc ttc tga ttt ccc ctc ccc cag ggc tca
3360
ttt tcc ccc ttt ttc ctg tac aca tcc ctg tct acc tcc tct cac cct gcc aca gat tct
3420
tcc tat cac aca ggg atg cca gtt gta ttt gtg gg 3455

Predicted Protein Sequence of Human ABCG4 Transporter

GPSGACKST	LSGGORK	VMFEDEPT	Transmembrane domains are underline
Walker A	C signature	Walker B	

ClustalW Multiple Sequence Alignment of the Members of the ABCG Subfamily

ABCG1	78	LSYSVPEGPWWRRKKGYKTLKGISGKFNSGELVAIMGPSGACKSTLMNLAGYRE-TG-MKGAVLINGLPRDLRCFRKVS
155		
ABCG4	66	LSYSVREGPCWRKRGYKTLKCLSGKFCRRELIGIMGPSGACKSTFMNLAGYRE-SG-MKGQILVNGRPRELRTFRKMS
143		
ABCG2	46	VKLKSGFLPCR-KPVEKEILSNINGIMKPG-LNAILCPTEGGKSSLLDVLAAKDPSPG-LSGDVLINGAPR-PANFCNS
121		
ABCG5	51	VRPWWDITSCR-QQWTRQILKDVSLYVESQIMCILGSSGCKTTLDDAMSGRLGRAGTFLGEVYVNGRALRREQFQDCF
129		
ABCG8	71	FKMPWTSPSCQ--NSCELGIONLSFKVRSQMLAIICSSGCGRASLLDVITGRGHGGKIKSGQIWINQOPSSPOLVRKC
148		

[illegible]

ABCG1	229	NNPPVMMFFDEPT	SGLDSASCFQVVSIMKGLAQGGRSIICTIHQPSAKLFELFDQLYVLSQGQCQVYRGKVCNLVPYLRDLG
308			
ABCG4	217	NNPPVMMFFDEPT	SGLDSASCFQVVSIMKSLAQGGRTIICTIHQPSAKLFEMFDKLYILSQGCICIFKGVVTNLIPYLKGLG
296			
ABCG2	202	TDPSILSLDEPT	TGLDSSTANAVLLLLKRMSKQGRTIIFSIHQPRYSIFKLFDSLTLTLASGRLMFHGPAQEALGYFESAG
281			
ABCG5	209	QDPKVMLFDEPT	TGLDCMTANQIVVLLVELARRNRIVVLTIIHQPRSELFQLFDKIAILSFGELIFCGTPAEMLDFFNDCG
288			
ABCG8	229	WNPGIILILDEPT	SGLDSFTAHLNVKTL SRLAKGNRLVLISLHQPRSDIFRLFDLVLLMTSGTPIYLGAAQHMVQYFTAIG
308			

ABCG1	309	LNCPTYHNPADFVMEVASGEYGD--QN-SRLVRAVREGMCDSDHKRD LGGDAEVNPF LWHRPSEEVKQTKRLKGLRKDS-
	384	
ABCG4	297	LHCPTYHNPADFIIEVASGEYGD--LN-PMLFRAVQNGLCAMA EK-----KSSPEKNEVPAPCPPCPPE-
	357	
ABCG2	282	YHCEAYNNPADFFLDIINGDSTAVALNREEDFKATEIIEPSKQDKP-LIEKLA EIVNSSFYKETKAE LHQLSGGEKKKK
	360	

FIGURE 4B

ABCG5 289 YPCPEHSNPFDFYMDLTSVDTQSKERE-IETSKRVQMIESAYKKS-----AICHKTLKNIERMKHLKTLF-
352
ABCG8 309 YPCPRYSNPADFYDLTSIDRRSREQE-LATREKAQSLAALFLEKVR-----DLDDFLWKAETKDLDEDTCESSVTPLD
382
: : : .

ABCG1 385 SSMEGCHSFASCLTQFCILFKRTFLSIMRDSVLTHLRITSHIGIGLLIGLLYLIGINETKK--VLSNSGFLFFSMLFLM
462
ABCG4 358 VDPIESHTFATSTLTQFCILFKRTFLSILRDTVLTHLRFMSHVIVIGVLIGLLYLHIGDDASK--VFNNTGCLFFSMLFLM
435
ABCG2 361 ITVFKEISYTTSFCHQLRWVSKRSFKNLLGNPQASIAQIIVTVVLGLVIGAIYFGLKNDSTG--IQNRAGVLFLLTTNQC
438
ABCG5 353 MVPFKTKD-SPGVFSKLGVLRRVTRNLVRNKLAVITRLLQNLIMGLFLLFFVLVRNSVLKGAIQDRVGLLYQFVGATP
431
ABCG8 383 TNCLPSPTKMPGAVQQFTTLIRRQISNDFRDLPDLLIHGAEACLSMTIGFLYFGHSGIQLS--FMDTAALLFMIGALIP
460
: : : .

ABCG1 463 FAALMPTVLTFFPLEMGVFLREHLNYWYSLKAYYLAKTMADVFPQIMFP-VAYCSIVYWMTSQPSDAVRVFLAALGTMTS
541
ABCG4 436 FAALMPTVLTFFPLEMAVFMREHLNYWYSLKAYYLAKTMADVFPQVVCV-VVYCSIVYWMTGQPAETSRFLFSALATATA
514
ABCG2 439 FSSVS-AVELFVVEKKLFIHEYISGYRVSSYFLGKLLSDLLPMPMLPSIIFTCIVYFMLGLKPKADAFFVMMFTLMMVA
517
ABCG5 432 YTGMLNAVNLPVPLRAVSDQESQDGLYQKWOMMLAYALHVLFPFSVVAT-MIFSSVCYWTGLHPEVARFGYFSAALLAPH
510
ABCG8 461 FNVILDVISKYSERAMLYYELEDGLYTTGPYFFAKILGELPEHCAYI-IIYGMPTYWLANLRPGLQPFLHFLVWLVV
539
: : : .

ABCG1 542 LVAQSLGLLIG-AASTSLQVATFVGVPVTAIPVLLFSGFFVSFDTIPTYLQWMSYISYVRYGFEGVILSIYG-----L
612
ABCG4 515 LVAQSLGLLIG-AASNSLQVATFVGVPVTAIPVLLFSGFFVSFKTIPTYLQWSSYLSYVRYGFEGVILTIYG-----M
585
ABCG2 518 YSASSMALAIA-AGQSVSVATLLMTICFVMMIFSGLLVNLTITASWLSWLQYFSIPRYGFTALQHNEFLGQNFPCPLN
596
ABCG5 511 LIGEFLLVLLGIVQNPNIIVNSVVALLSIAGVLVGSGFLRNIQEMPIPFKIIISYFTFQKYCSEILVNEFYGLN---FTC
587
ABCG8 540 FCCRIMALAAA-ALLPTFHMAFFSNALYNSFYLAGGFMINLSSLWTPAWISKVSFLRWCFEGLMKIQFS-----R
610
: : : .

ABCG1 613 DREDLHCDIDETCHFQ-KSEAILRELDVENAKLYLDFIVLGIFFISLRLLIAYLVLRKYKIRAER 674
ABCG4 586 ERGDLTC-LEERCPPR-EPQSILRALDVEDAKLYMDFVLGIFFLALRLLAYLVLRVVKSER 646
ABCG2 597 ATGNNPC-NYATCTG--EYLVKQIGIDLSPWGLWKNHVALACMIVIFLTIAYLKLLFLKKYS 655
ABCG5 588 GSSNVSVTTNPMCAFTQGIQIEKTCPGATSRFTMNFILYSFIPALVILGIVVFKIRDHLIS 651
ABCG8 611 RTYKMPLGNLTIASV---GDKILSMELDSYPLYAIYLIVIGLSGGFMVLYYVSLRFIKQKPSQDW 673
: : : .

ClustalW Multiple Sequence Alignment of Partial Human ABCG4 Transporter in GenBank
(AN: CAC17140) and Human ABCG4 Transporter of this Invention

[illegible]

ABCG4	81	YKTLKCLSGKFCRRELIGIMCPSGAGKSTFMNLAGYRESGMKGQILVNGRPRELRTFRKMSCYIMQDDMLLPHLTVLE
160		
CAC17140	62	YKTLKCLSGKFCRRELIGIMCPSGAGKSTFMNLAGYRESGMKGQILVNGRPRELRTFRKMSCYIMQDDMLLPHLTVLE
141		
.....		

	ABCG4	161	AMMVSANLNLTENPDVKNDLVTEILTALGLMSCSHTRTALLSGGQRRLAIALELNNPPVMEFDEPTSGLDASACFOVV
	[240]		
	CAC17140	142	AMMVSANKLKSEKQEVKKELVTETALTALGLMSCSHTRTALLSGGQRRLAIALELNNPPVMEFDEPTSGLDASACFOVV
	[221]		
			::::: .:. :.. :::::::::::::::::::::

ABCG4	241	SLMKSLAQGGRTIICTIHQPSAKLFEMFDKLYILSQGQCIFKGVVTNLIPYLKGLGLHCPTYHNPADFTIEVASGEYGD
320		
CAC17140	222	SLMKSLAQGGRTIICTIHQPSAKLFEMFDKLYILSQGQCIFKGVVTNLIPYLKGLGLHCPTYHNPADFTIEVASGEYGD
301		
	

ABC	4	321	NPMLFRAVQNGLCAMAEKKSSPEKNEVPAPCPPCPPEVDPIESHTFATSTLTQFCILFKRTFLSILRDTVLTHLRFMSHV
400			
CAC	17140	302	NPMLFRAVQNGLCAMAEKKSSPEKNEVPAPCPPCPPEVDPIESHTFATSTLTQFCILFKRTFLSILRDTVLTHLRFMSHV
381			
		

ABCG4	401	VIGVLIGLLYLHIGDDASKVFNNNTGCLFFSMLFLMFAALMPTVLTFTPLEMAVFMREHLNYWYSLKAYYLAKTMADVPPQV
480		
CAC17140	382	VIGVLIGLLYLHIGDDASKVFNNNTGCLFFSMLFLMFAALMPTVLTFTPLEMAVFMREHLNYWYSLKAYYLAKTMADVPPQV
461		
.....		

ABCG4	481	VCPVVYCSIVYWMTGQPAETS	RFLLFSALATAT	VAQSLGLLIGAASN	SLQVATFVGPVTAIPVLLFSGFFV	SFKTIPT
560						
CAC17140	462	VCPVVYCSIVYWMTGQPAETS	RFLLFSALATAT	VAQSLGLLIGAASN	SLQVATFVGPVTAIPVLLFSGFFV	SFKTIPT
541						

[illegible]

ABCG4	641	RVKSER	646
CAC17140	622	RVKSER	627
	:	:	:

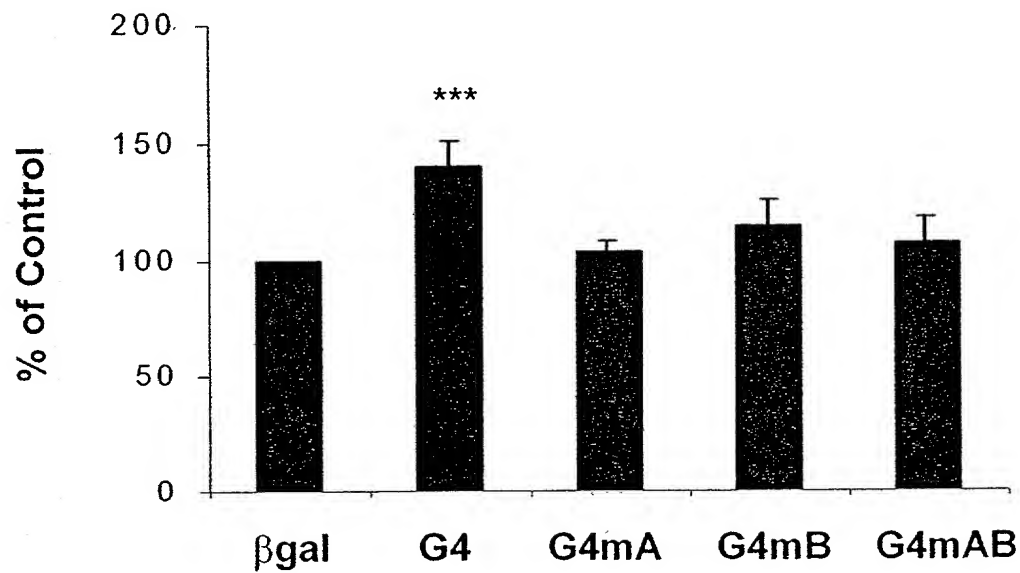


Figure 6

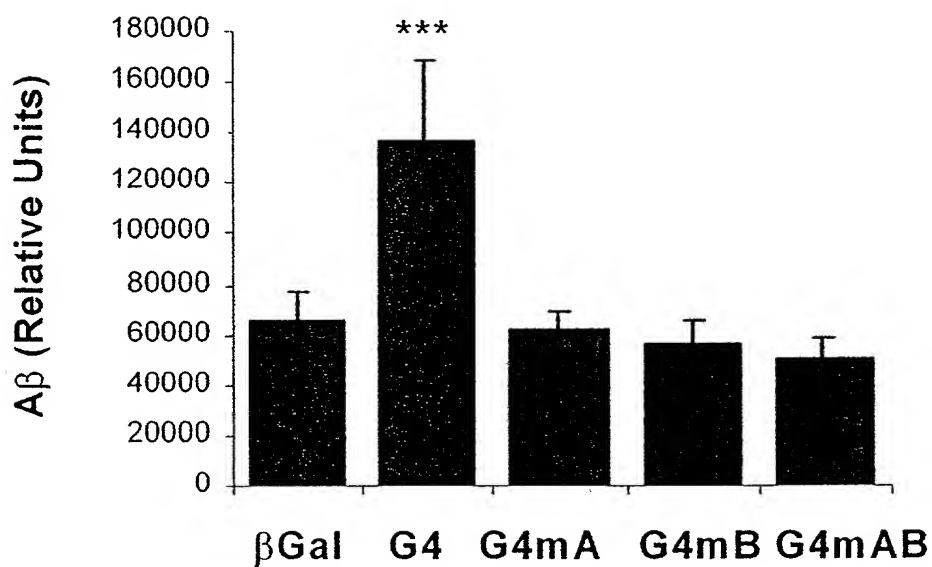


Figure 7

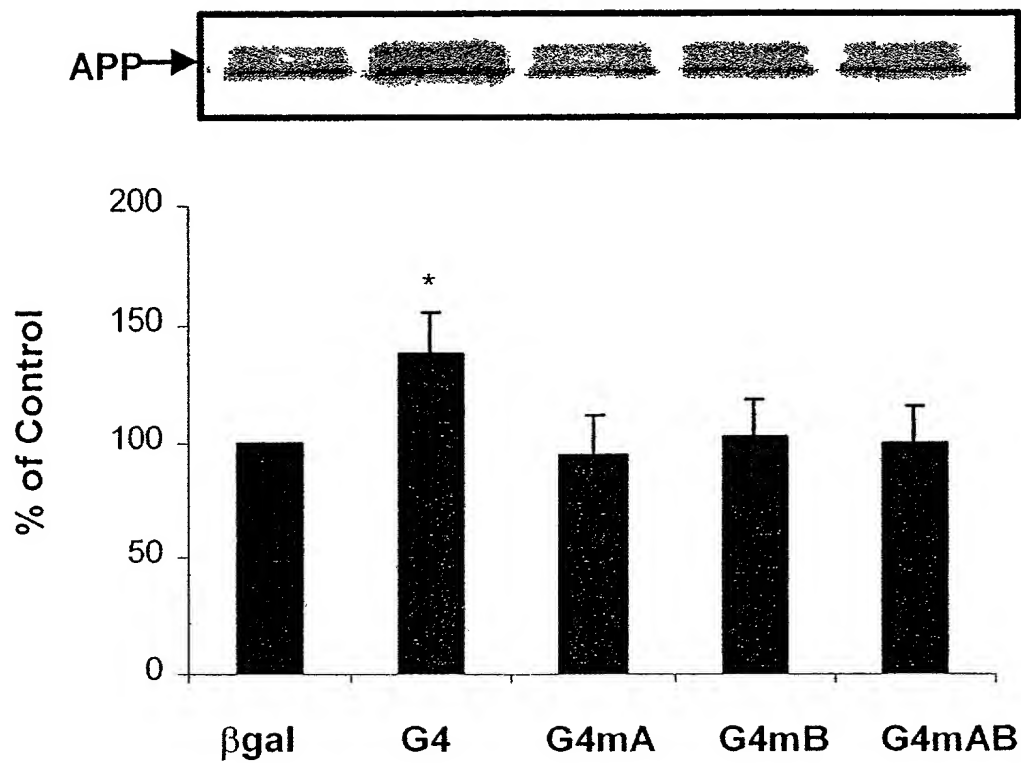


Figure 8

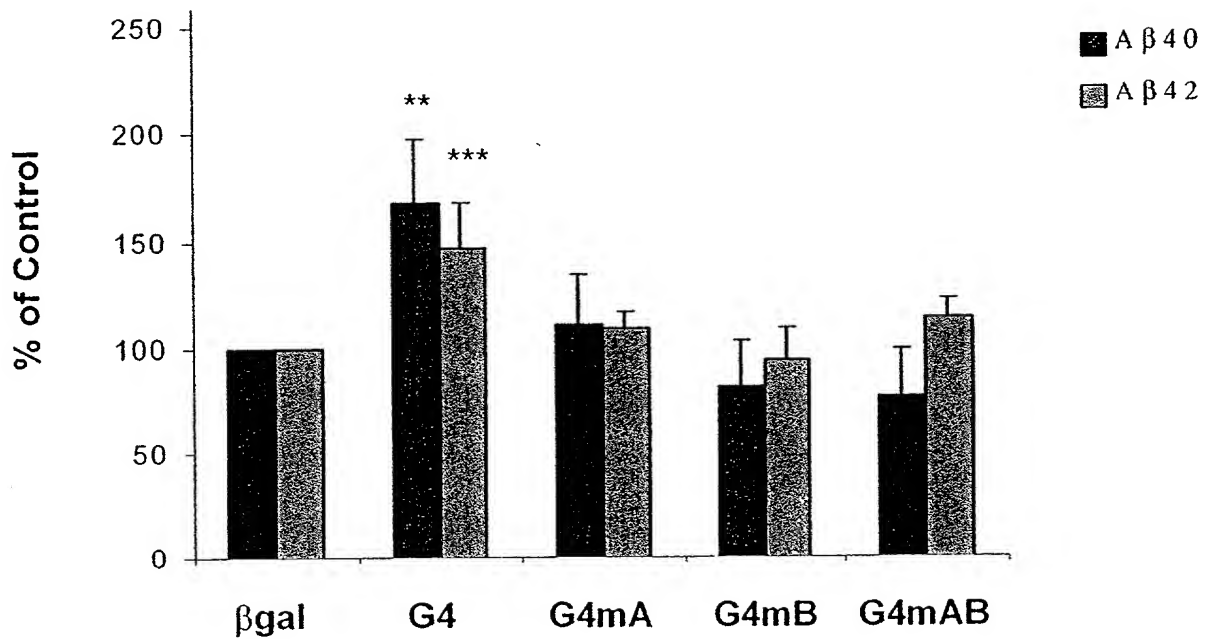


Figure 9

Directory: Mapleleaf/target clone/ABCG family/abcg4/g4cdna (Assembly file)

G4-clone nucleotide sequence range 1 to 2687

TACCGAGCTCGGATCCACTAGTCCAGTGTGGTGGAAATTGCCCTTGCCACCATGCGGAGAGAAGGCGCTGGAGG
CCGTGGGCTGTGGACTAGGGCCGGGGCTGTGGCCATGGCCGTGACGCTGGAGGACGGGCGGAACCCCTG
TGCTGACCACGCACCTGAAGAAGGTGGAGAACCACATCACTGAAGCCAGCGCTTCTCCACCTACCCAAGC
GCTCAGCCGTGGACATCGAGTTCTGTGGAGCTGTCTATTCCGTGCGGGAGGGGCCCTGCTGGCGCAAAAGGG
GTTATAAGACCCTTCTCAAGTGCCTCTCAGGTAAATTCTGCCGCCGGGAGCTGATTGGCATCATGGGCCCT
CAGGGGCTGGCAAGTCTACATTCTGAACATCTTGGCAGGATACAGGGAGTCTGGAATGAAGGGGCAGATCC
TGGTTAATGGAAGGCCACGGGAGCTGAGGACCTTCCGCAAGATGTCCTGCTACATCATGAAGATGACATGC
TGCTGCCGCACCTCACGGTGTGGAAGCCATGATGGTCTCTGCTAACCTGAAGCTGAGTGAGAAGCAGGAGG
TGAAGAAGGAGCTGGTGACAGAGATCCTGACGGCACTGGGCTGATGTGCTGCTCCCGCACGAGGACAGCCC
TGCTCTCTGGCGGGCAGAGGAAGCGTCTGGCCATCGCCCTGGAGCTGGTCAACAACCCGCCTGTCTGTTCT
TTGATGAGCCCACAGTGGTCTGGATAGCGCTCTTGTTCAGGTGGTGTCCCTCATGAAGTCCCTGGCAC
AGGGGGGCGCTACCATCATCTGCACCATCCACAGCCAGTGCCAAGCTCTTTGAGATGTTTGACAAGCTCT
ACATCCTGAGCCAGGGTCAGTGCATCTTCAAAGCGTGGTCACCAACCTGATCCCCTATCTAAAGGGACTCG
GCTTGCAATTGCCCCACCTACCACAACCCGGCTGACTTCATCATCGAGGTGGCCTCTGGCGAGTATGGAGACC
TGAACCCCATGTTGTTTCAGGGCTGTGCAGAAATGGGCTGTGCGCTATGGCTGAGAAGAAGAGCAGCCCTGAGA
AGAACGAGGTCCCTGCCCCATGCCCTCCTTGCTCCGGAAGTGGATCCCATTGAAAGCCACACCTTTGCCA
CCAGCACCTCACACAGTCTGCATCCTCTTCAAGAGGACCTTCCTGTCCATCCTCAGGGACACGGTCTGA
CCCACCTACGGTTCATGTCCCACGTGGTTATTGGCGTGCTCATCGGCCTCCTCTACCTGCATATTGGCGACG
ATGCCAGCAAGGTCTTCAACAACACCGGCTGCCTCTTCTTCCATGCTGTTCCCTCATGTTCCGCGCCCTCA
TGCCAACTGTGCTCACCTTCCCTTAGAGATGGCGGTCTTCATGAGGGAGCACCTCAACTACTGGTACAGCC
TCAAAGCGTATTACCTGGCCAAGACCATGGCTGACGTGCCCTTTCAGGTGGTGTGTCCGGTGGTCTACTGCA
GCATTGTGTACTGGATGACGGGCCAGCCCGCTGAGACCAGCCGCTTCTGCTCTTCTCAGCCCTGGCCACCG
CCACCGCCTTGGTGGGCCAATCTTTGGGGCTGCTGATCGGAGCTGCTTCCAACCTCCCTACAGGTGGCCACTT
TTGTGGGGCCAGTTACCGCCATCCCTGTCTCTTGTCTCCGGCTTCTTTGTGACGTTCAAGACCATCCCCA
CTTACCTGCAATGGAGCTCCTATCTCTCTATGTGAGGTATGGCTTTGAGGGTGTGRTCTGACGATCTATG
GCATGGAGCGAGGAGACCTGACATGTTTAGAGGAACGCTGCCMGTTCCGGGAGCCACAGAGCATCCTCCGAG
CGCTGGATGTGGAGGATGCCAAGCTCTACATGGACTTCCTGGTCTTGGGCATCTTCTTCTAGCCCTGCGGC
TGCTGGCCTACCTTGTGCTGCGTTACCGGGTCAAGTCAGAGAGATGAGGCTTGCCCCAGCCTGTACCCCAG
CCCCTGCAGCAGGAAGCCCCCAGTCCCAGCCCTTGGGACTGTTTAACTTATAGACTTGGGCACTGGTTC
CTGGCGGGGCTATCCTCTCCTCCCTTGGCTCCTCCACAGGCTGGCTGTGCGACTGCGCTCCCAGCCTGGGCT
CTGGGAGTGGGGGCTCCAGCCCTCCCCTATGCCCAGGAGTCTTCCAAGTTGATGCGGTTTGTAGCTTCC
TCCCTACTCTCTCCAACACCTGCATGCAAAGACTACTGGGAGGCTGCTGCCTCCTTCTGCCCATGGCACCC
TCCTCTGCTGTCTGCCTGGGAGCCCTAGGCTCTTAGGGCCCCACTTACAAGTACCAAAGTGGCCCCCTCT
KGGGGTCCCCACCACACAAGTGTGTTGTAAGTGGGCTGCTATAAGGTTGGAGTTCAGGGCTGGGCCCTGGT
GGAGTCCACTGGAAGTCCCATCATGGATGTTGAAATGGACAGGGAAGGACTCTGGAAGTCTTCTCCTCTCC
TCCTCTTCTCTCCACCCCTAGACCTGGCTGACTTGACAATCTGCCAGGACAGAAGCTGGGGTTTTCTGTC
TAGGTCAACACTCCCAATCCTGGGGGRTTGGAGRGGCTGGGGSTGTGGGRTGSCCATCCCCCTCCCCATC
ACCTTTGGTGGGGGSAGGGCCTG

Figure 10

G4-clone polypeptide sequence range 1 to 646

MAEKALEAVGCGLGPGAVAMAVTLEDGAEPVLTTHLKKVENHITEAQRFSLPKRSAVD
IEFVELSYSVREGPCWRKRGYKTLKCLSGKFCRRELIGIMGPSGAGKSTFMNILAGYRE
SGMKGQILVNGRPRELRTFRKMSCYIMQDDMLLPHLTVLEAMMVSANLKLSEKQEVKKEL
VTEILTALGLMSCSRTRTALLSGGQQRKRLAIALELVNNPPVMFFDEPTSGLDSASCFQVV
SLMKSLAQGGRTIICTIHQPSAKLFEMFDKLYILSQGQCIFKGVVTNLIPLYLKGLGLHCP
TYHNPADFIIEVASGEYGDLPMLFRAVQNGLCAMAEKKSSPEKNEVPAPCPPCPPEVDP
IESHTFATSTLTQFCILFKRTFLSILRDTVLTHLRFMSHVIGVLIGLLYLHIGDDASKV
FNNTGCLFFSMLFLMFAALMPTVLTFFLEMAVFMREHLNYWYSLKAYYLAKTMADVFPQV
VCPVYCSIVYWMTGQPAETSRFLLEFALATATALVAQSLGLLIGAASNSLQVATFVGVPV
TAIPVLLFSGFFVSEFKTIPTYLQWSSYLSYVRYGFEGVXLTIIYGMERGDLTCLEERCXFR
EPQSILRALDVEDAKLYMDFLVLGIFFLALRLLAYLVLRYRVKSER

Figure 11